

**Practitioner's Docket No. MPI00-343P1RM****IN THE SPECIFICATION**

At page 27, first full paragraph, please replace paragraph with the following text to remove browser executable code:

The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch (*J. Mol. Biol.* (48):444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package (available at <http://www.gcg.com>) ~~www.gcg.com~~), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (available at <http://www.gcg.com>) ~~www.gcg.com~~), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. A preferred, non-limiting example of parameters to be used in conjunction with the GAP program include a Blossum 62 scoring matrix with a gap penalty of 12, a gap extend penalty of 4, and a frameshift gap penalty of 5.

At page 27, last paragraph through top of page 28 replace the paragraph with the following text to remove browser executable code:

The nucleic acid and protein sequences of the present invention can further be used as a "query sequence" to perform a search against public databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to ACTR-1 nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to ACTR-1 protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See <http://www.ncbi.nlm.nih.gov> ~~www.ncbi.nlm.nih.gov~~.

At page 80, last paragraph, through page 81 top of the page please replace the paragraph with the following text to remove browser executable code:

The amino acid sequence of human ACTR-1 was analyzed using the program PSORT (<http://www.psort.nibb.ac.jp>) ~~(www.psort.nibb.ac.jp)~~ to predict the localization of the proteins within the cell. This program assesses the presence of different targeting and localization amino acid sequences within the query sequence. The results of the analyses show that human ACTR-1 may be localized to the

**Practitioner's Docket No. MPI00-343P1RM**

nucleus, to the mitochondria, or to the cytoplasm. Based on homology to mouse and rat GPATS, human APCR-1 is believed to be mitochondrial.